

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Regents of the University of Minnesota
- (ii) TITLE OF THE INVENTION: ANALYSIS OF ALPHA INTEGRINS
FOR THE DIAGNOSIS OF DIABETIC NEPHROPATHY
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Merchant & Gould
(B) STREET: 3100 Norwest Center
90 South 7th Street
(C) CITY: Minneapolis
(D) STATE: MN
(E) COUNTRY: US
(F) ZIP: 55402
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: Unknown
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Kettelberger, Denise
(B) REGISTRATION NUMBER: 33,924
(C) REFERENCE/DOCKET NUMBER: 600.314USWO
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 612-332-5300
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(C) TELEX:

102050-40000050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAG TGT CCG GTT GGG AGA GAG AGA GCA ATG CCT TGC GTG AAG TTG GAC 707
Lys Cys Pro Val Gly Arg Glu Arg Ala Met Pro Cys Val Lys Leu Asp
55 60 65

TTG	CCA	GTT	AAC	ACA	TCG	ATC	CCC	AAT	GTC	ACA	GAA	ATA	AAG	GAA	AAC	755
Glu	Pro	Val	Asn	Thr	Ser	Ile	Pro	Asn	Val	Thr	Glu	Ile	Lys	Glu	Asn	
70						75					80					
ATG	ACA	TTT	GGA	TCA	ACT	TTA	GTC	ACC	AAC	CCG	AAT	GGA	GGA	TTT	CTG	803
Met	Thr	Phe	Gly	Ser	Thr	Leu	Val	Thr	Asn	Pro	Asn	Gly	Gly	Phe	Leu	
85					90					95					100	
GCA	TGT	GGG	CCC	TTG	TAT	GCC	TAT	AGA	TGT	GGA	CAT	TTG	CAT	TAT	ACA	851
Ala	Cys	Gly	Pro	Leu	Tyr	Ala	Tyr	Arg	Cys	Gly	His	Leu	His	Tyr	Thr	
				105					110					115		
ACT	GGA	ATA	TGT	TCT	GAT	GTC	AGT	CCT	ACA	TTT	CAA	GTT	GTG	AAC	TCC	899
Thr	Gly	Ile	Cys	Ser	Asp	Val	Ser	Pro	Thr	Phe	Gln	Val	Val	Asn	Ser	
			120					125					130			
TTT	GCC	CCT	GTA	CAA	GAA	TGC	AGC	ACC	CAG	CTG	GAC	ATA	GTC	ATC	GTC	947
Phe	Ala	Pro	Val	Gln	Glu	Cys	Ser	Thr	Gln	Leu	Asp	Ile	Val	Ile	Val	
		135					140					145				
CTG	GAT	GGC	TCC	AAC	AGC	ATC	TAC	CCC	TGG	GAA	AGT	GTC	ATC	GCC	TTT	995
Leu	Asp	Gly	Ser	Asn	Ser	Ile	Tyr	Pro	Trp	Glu	Ser	Val	Ile	Ala	Phe	
	150					155					160					
TTA	AAC	GAC	CTT	CTT	AAG	AGG	ATG	GAT	ATT	GGC	CCT	AAG	CAG	ACA	CAG	1043
Leu	Asn	Asp	Leu	Leu	Lys	Arg	Met	Asp	Ile	Gly	Pro	Lys	Gln	Thr	Gln	
165					170					175					180	
GTC	GGG	ATT	GTA	CAG	TAT	GGA	GAG	AAT	GTA	ACC	CAT	GAG	TTC	AAC	CTC	1091
Val	Gly	Ile	Val	Gln	Tyr	Gly	Glu	Asn	Val	Thr	His	Glu	Phe	Asn	Leu	
				185					190					195		
AAT	AAG	TAT	TCA	TCC	ACA	GAA	GAG	GTC	CTT	GTC	GCA	GCA	AAC	AAA	ATA	1139
Asn	Lys	Tyr	Ser	Ser	Thr	Glu	Glu	Val	Leu	Val	Ala	Ala	Asn	Lys	Ile	
			200					205					210			
GGC	CGA	CAG	GGA	GGC	CTC	CAA	ACG	ATG	ACA	GCC	CTT	GGA	ATA	GAC	ACA	1187
Gly	Arg	Gln	Gly	Gly	Leu	Gln	Thr	Met	Thr	Ala	Leu	Gly	Ile	Asp	Thr	
		215					220					225				
GCC	AGG	AAA	GAG	GCA	TTC	ACT	GAA	GCT	CGG	GGT	GCC	AGG	AGG	GGA	GTT	1235
Ala	Arg	Lys	Glu	Ala	Phe	Thr	Glu	Ala	Arg	Gly	Ala	Arg	Arg	Gly	Val	
	230					235					240					
AAA	AAA	GTC	ATG	GTT	ATT	GTG	ACC	GAC	GGA	GAA	TCG	CAT	GAC	AAC	TAT	1283
Lys	Lys	Val	Met	Val	Ile	Val	Thr	Asp	Gly	Glu	Ser	His	Asp	Asn	Tyr	
245					250					255					260	
CGC	TGA	AAC	AGG	TCA	TCC	AAG	ACT	GCG	AGG	ACG	AAA	ACA	TTC	AGC	GAT	1331
Arg	Leu	Lys	Gln	Val	Ile	Gln	Asp	Cys	Glu	Asp	Glu	Asn	Ile	Gln	Arg	
				265					270					275		
TTT	TCC	ATA	GCT	ATC	CTT											

GAA AAA TTT GTG GAG GAA ATA AAA TCG ATC GCA AGC GAG CCC ACG GAA	1427
Glu Lys Phe Val Glu Glu Ile Lys Ser Ile Ala Ser Glu Pro Thr Glu	
295 300 305	
AAG CAC TTC TTC AAT GTC TCG GAT GAG TTG GCC CTG GTC ACT ATT GTT	1475
Lys His Phe Phe Asn Val Ser Asp Glu Leu Ala Leu Val Thr Ile Val	
310 315 320	
AAA GCT CTG GGA GAA AGG ATA TTC GCT TTG GAA GCG ACA GCT GAC CAG	1523
Lys Ala Leu Gly Glu Arg Ile Phe Ala Leu Glu Ala Thr Ala Asp Gln	
325 330 335 340	
TCA GCA GCT TCA TTT GAG ATG GAA ATG TCT CAG ACT GGC TTC AGT GCT	1571
Ser Ala Ala Ser Phe Glu Met Glu Met Ser Gln Thr Gly Phe Ser Ala	
345 350 355	
CAC TAC TCC CAG GAC TGG GTC ATG CTT GGA GCG GTG GGA GCC TAT GAC	1619
His Tyr Ser Gln Asp Trp Val Met Leu Gly Ala Val Gly Ala Tyr Asp	
360 365 370	
TGG AAC GGA ACT GTG GTC ATG CAG AAG GCT AAC CAG ATG GTC ATC CCT	1667
Trp Asn Gly Thr Val Val Met Gln Lys Ala Asn Gln Met Val Ile Pro	
375 380 385	
CAT AAC ACC ACC TTT CAA ACT GAG CCC GCC AAG ATG AAC GAG CCT CTG	1715
His Asn Thr Thr Phe Gln Thr Glu Pro Ala Lys Met Asn Glu Pro Leu	
390 395 400	
GCT TCT TAT TTA GGT TAC ACA GTG AAC TCG GCC ACC ATC CCT GGA GAT	1763
Ala Ser Tyr Leu Gly Tyr Thr Val Asn Ser Ala Thr Ile Pro Gly Asp	
405 410 415 420	
GTG CTC TAC ATC GCT GGG CAG CCT CGG TAC AAT CAT ACG GGC CAG GTC	1811
Val Leu Tyr Ile Ala Gly Gln Pro Arg Tyr Asn His Thr Gly Gln Val	
425 430 435	
GTC ATC TAC AAG ATG GAG GAT GGG AAC ATC AAC ATT CTG CAG ACA CTC	1859
Val Ile Tyr Lys Met Glu Asp Gly Asn Ile Asn Ile Leu Gln Thr Leu	
440 445 450	
GGC GGA GAG CAG ATT GGT TCC TAC TTT GGT AGT GTC TTA ACA ACA ATT	1907
Gly Gly Glu Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Thr Thr Ile	
455 460 465	
GAC ATC GAC AAA GAT TCT TAT ACT GAT CTG CTT CTC GTC GGG GCC CCC	1955
Asp Ile Asp Lys Asp Ser Tyr Thr Asp Leu Leu Leu Val Gly Ala Pro	
470 475 480	
ATG TAC ATG GGG ACA GAG AAA GAG GAA CAG GGC AAG GTG TAC GTG TAC	2003
Met Tyr Met Gly Thr Glu Lys Glu Glu Gln Gly Lys Val Tyr Val Tyr	
485 490 495 500	
GCT GTG AAT CAG ACA AGG TTT GAA TAT CAA ATG AGC CTG GAA CCA ATT	2051
Ala Val Asn Gln Thr Arg Phe Glu Tyr Gln Met Ser Leu Glu Pro Ile	
505 510 515	

0900000004-05000001

GGC AGA CCT GCT GCT CAT CCC TGA AGG ATA ATT CAT GCA CGA AAG AAA	2099
Arg Gln Thr Cys Ser Ser Leu Lys Asp Asn Ser Cys Thr Lys Glu	
520 525 530	
AAC AAG AAT GAG CCC TGC GGG GCC CGC TTC GGA ACA GCA ATT GCT GCT	2147
Asn Lys Asn Glu Pro Cys Gly Ala Arg Phe Gly Thr Ala Ile Ala Ala	
535 540 545	
GTA AAA GAC CTC AAC GTG GAT GGA TTT AAT GAC GTC GTG ATT GGA GCT	2195
Val Lys Asp Leu Asn Val Asp Gly Phe Asn Asp Val Val Ile Gly Ala	
550 555 560	
CCG CTG GAA GAT GAC CAC GCA GGA GCT GTG TAC ATT TAT CAT GGC AGT	2243
Pro Leu Glu Asp Asp His Ala Gly Ala Val Tyr Ile Tyr His Gly Ser	
565 570 575 580	
GGC AAG ACC ATA AGG GAG GCG TAT GCA CAA CGC ATT CCA TCA GGT GGG	2291
Gly Lys Thr Ile Arg Glu Ala Tyr Ala Gln Arg Ile Pro Ser Gly Gly	
585 590 595	
GAT GGC AAG ACC CTG AAA TTT TTC GGC CAG TCT ATC CAC GGA GAG ATG	2339
Asp Gly Lys Thr Leu Lys Phe Phe Gly Gln Ser Ile His Gly Glu Met	
600 605 610	
GAT TTA AAT GGT GAC GGT CTG ACT GAC GTG ACC ATT GGA GGC CTT GGT	2387
Asp Leu Asn Gly Asp Gly Leu Thr Asp Val Thr Ile Gly Gly Leu Gly	
615 620 625	
GGA GCA GCC CTC TTC TGG GCC AGA GAT GTG GCT GTA GTT AAA GTG ACC	2435
Gly Ala Ala Leu Phe Trp Ala Arg Asp Val Ala Val Val Lys Val Thr	
630 635 640	
ATG AAT TTT GAA CCC AAT AAA GTG AAT ATT CAA AAG AAA AAC TGC CGT	2483
Met Asn Phe Glu Pro Asn Lys Val Asn Ile Gln Lys Lys Asn Cys Arg	
645 650 655 660	
GTG GAG GGC AAA GAA ACA GTG TGC ATA AAT GCT ACA ATG TGT TTT CAT	2531
Val Glu Gly Lys Glu Thr Val Cys Ile Asn Ala Thr Met Cys Phe His	
665 670 675	
GTG AAA TTA AAG TCT AAA GAG GAC TCA ATT TAC GAG GCT GAT CTG CAG	2579
Val Lys Leu Lys Ser Lys Glu Asp Ser Ile Tyr Glu Ala Asp Leu Gln	
680 685 690	
TAC CGT GTC ACC CTT GAT TCA CTG AGG CAG ATA TCA CGG AGC TTT TTT	2627
Tyr Arg Val Thr Leu Asp Ser Leu Arg Gln Ile Ser Arg Ser Phe Phe	
695 700 705	
TCT GGA ACT CAG GAA AGG AAG ATT CAA AGA AAT ATC ACC GTT CGA GAA	2675
Ser Gly Thr Gln Glu Arg Lys Ile Gln Arg Asn Ile Thr Val Arg Glu	
710 715 720	
TCA GAA TGC ATC AGG CAC TCC TTC TAC ATG TTG GAC AAA CAT GAC TTT	2723
Ser Glu Cys Ile Arg His Ser Phe Tyr Met Leu Asp Lys His Asp Phe	
725 730 735 740	

CAG GAC TCT GTG AGA GTG ACT CTG GAT TTT AAT CTC ACT GAT CCA GAA	2771
Gln Asp Ser Val Arg Val Thr Leu Asp Phe Asn Leu Thr Asp Pro Glu	
745 750 755	
AAT GGT CCT GTA CTT GAT GAC GCT CTG CCA AAC TCA GTC CAC GAA CAC	2819
Asn Gly Pro Val Leu Asp Asp Ala Leu Pro Asn Ser Val His Glu His	
760 765 770	
ATT CCC TTT GCC AAA GAC TGT GGA AAC AAG GAA AGA TGC ATT TCA GAC	2867
Ile Pro Phe Ala Lys Asp Cys Gly Asn Lys Glu Arg Cys Ile Ser Asp	
775 780 785	
CTC ACT CTG AAT GTG TCC ACC ACA GAA AAG AGC CTG CTG ATC GTC AAG	2915
Leu Thr Leu Asn Val Ser Thr Thr Glu Lys Ser Leu Leu Ile Val Lys	
790 795 800	
TCC CAG CAT GAC AAG TTC AAC GTT AGC CTC ACC GTC AAA AAC AAA GGA	2963
Ser Gln His Asp Lys Phe Asn Val Ser Leu Thr Val Lys Asn Lys Gly	
805 810 815 820	
GAC AGT GCG TAC AAC ACC AGG ACA GTG GTG CAG CAT TCA CCA AAT CTG	3011
Asp Ser Ala Tyr Asn Thr Arg Thr Val Val Gln His Ser Pro Asn Leu	
825 830 835	
ATT TTT TCG GGA ATT GAG GAG ATC CAA AAA GAT AGC TGT GAA TCT AAT	3059
Ile Phe Ser Gly Ile Glu Glu Ile Gln Lys Asp Ser Cys Glu Ser Asn	
840 845 850	
CAA AAT ATC ACT TGC AGA GTT GGA TAT CCT TTC CTA AGA GCA GGA GAA	3107
Gln Asn Ile Thr Cys Arg Val Gly Tyr Pro Phe Leu Arg Ala Gly Glu	
855 860 865	
ACG GTT ACC TTC AAA ATA ATA TTC CAG TTT AAC ACA TCC CAT CTC TCG	3155
Thr Val Thr Phe Lys Ile Ile Phe Gln Phe Asn Thr Ser His Leu Ser	
870 875 880	
GAA AAT GCA ATC ATT CAC TTA AGT GCA ACA AGT GAC AGT GAG GAG CCC	3203
Glu Asn Ala Ile Ile His Leu Ser Ala Thr Ser Asp Ser Glu Glu Pro	
885 890 895 900	
CTG GAA TCT CTT AAT GAT AAT GAA GTA AAT ATT TCC ATC CCA GTA AAA	3251
Leu Glu Ser Leu Asn Asp Asn Glu Val Asn Ile Ser Ile Pro Val Lys	
905 910 915	
TAT GAA GTT GGA CTG CAG TTT TAC AGT TCT GCG AGT GAA CAT CAC ATT	3299
Tyr Glu Val Gly Leu Gln Phe Tyr Ser Ser Ala Ser Glu His His Ile	
920 925 930	
TCA GTC GCT GCC AAT GAG ACG ATC CCT GAG TTT ATT AAC TCC ACT GAG	3347
Ser Val Ala Ala Asn Glu Thr Ile Pro Glu Phe Ile Asn Ser Thr Glu	
935 940 945	
GAC ATT GGG AAT GAA ATT AAT GTC TTC TAT ACG ATT AGA AAG AGG GGG	3395
Asp Ile Gly Asn Glu Ile Asn Val Phe Tyr Thr Ile Arg Lys Arg Gly	
950 955 960	

CAT TTC CCA ATG CCA GAA CTT CAG CTG TCA ATT TCA TTC CCC AAT TTG His Phe Pro Met Pro Glu Leu Gln Leu Ser Ile Ser Phe Pro Asn Leu 965 970 975 980	3443
ACG GCA GAT GGT TAT CCT GTA CTG TAC CCA ATT GGA TGG TCA TCT TCA Thr Ala Asp Gly Tyr Pro Val Leu Tyr Pro Ile Gly Trp Ser Ser Ser 985 990 995	3491
GAT AAT GTG AAC TGT AGA CCC CGG AGC CTT GAG GAC CCC TTT GGC ATC Asp Asn Val Asn Cys Arg Pro Arg Ser Leu Glu Asp Pro Phe Gly Ile 1000 1005 1010	3539
AAC TCT GGG AAG AAA ATG ACA ATA TCG AAG TCT GAG GTT CTC AAA AGA Asn Ser Gly Lys Lys Met Thr Ile Ser Lys Ser Glu Val Leu Lys Arg 1015 1020 1025	3587
GGC ACA ATC CAG GAC TGC AGT AGT ACG TGT GGA GTT GCC ACC ATC ACG Gly Thr Ile Gln Asp Cys Ser Ser Thr Cys Gly Val Ala Thr Ile Thr 1030 1035 1040	3635
TGT AGC CTC CTT CCT TCC GAC CTG AGT CAA GTG AAT GTC TCG CTC CTC Cys Ser Leu Leu Pro Ser Asp Leu Ser Gln Val Asn Val Ser Leu Leu 1045 1050 1055 1060	3683
CTG TGG AAA CCG ACT TTC ATA AGA GCA CAT TTT TCC AGC TTA AAC CTT Leu Trp Lys Pro Thr Phe Ile Arg Ala His Phe Ser Ser Leu Asn Leu 1065 1070 1075	3731
ACT CTA AGA GGA GAA CTT AAG AGT GAA AAT TCA TCG CTG ACT TTA AGT Thr Leu Arg Gly Glu Leu Lys Ser Glu Asn Ser Ser Leu Thr Leu Ser 1080 1085 1090	3779
AGC AGC AAC CGG AAG CGA GAG CTG GCT ATT CAG ATA TCC AAA GAC GGG Ser Ser Asn Arg Lys Arg Glu Leu Ala Ile Gln Ile Ser Lys Asp Gly 1095 1100 1105	3827
CTC CCA GGC AGA GTG CCG CTG TGG GTT ATC CTC CTG AGC GCC TTC GCG Leu Pro Gly Arg Val Pro Leu Trp Val Ile Leu Leu Ser Ala Phe Ala 1110 1115 1120	3875
GGG CTA CTG CTG CTA ATG CTC CTT ATA TTG GCT CTG TGG AAG ATT GGA Gly Leu Leu Leu Leu Met Leu Leu Ile Leu Ala Leu Trp Lys Ile Gly 1125 1130 1135 1140	3923
TTC TTC AAA AGG CCA CTG AAG AAG AAA ATG GAG AAA TGAAAGGTTT Phe Phe Lys Arg Pro Leu Lys Lys Lys Met Glu Lys 1145 1150	3969
CATAGAAAAA AAAAAAAAAA	3987

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Val Gly Ile Val Gln Tyr Gly Glu Asn Val Thr His Glu Phe Asn Leu
185 190 195

Asn	Lys	Tyr	Ser	Ser	Thr	Glu	Glu	Val	Leu	Val	Ala	Ala	Asn	Lys	Ile	
			200					205					210			
Gly	Arg	Gln	Gly	Gly	Leu	Gln	Thr	Met	Thr	Ala	Leu	Gly	Ile	Asp	Thr	
		215					220					225				
Ala	Arg	Lys	Glu	Ala	Phe	Thr	Glu	Ala	Arg	Gly	Ala	Arg	Arg	Gly	Val	
		230				235					240					
Lys	Lys	Val	Met	Val	Ile	Val	Thr	Asp	Gly	Glu	Ser	His	Asp	Asn	Tyr	
245					250					255					260	
Arg	Leu	Lys	Gln	Val	Ile	Gln	Asp	Cys	Glu	Asp	Glu	Asn	Ile	Gln	Arg	
				265					270					275		
Phe	Ser	Ile	Ala	Ile	Leu	Gly	His	Tyr	Asn	Arg	Gly	Asn	Leu	Ser	Thr	
			280					285					290			
Glu	Lys	Phe	Val	Glu	Glu	Ile	Lys	Ser	Ile	Ala	Ser	Glu	Pro	Thr	Glu	
		295					300					305				
Lys	His	Phe	Phe	Asn	Val	Ser	Asp	Glu	Leu	Ala	Leu	Val	Thr	Ile	Val	
		310				315					320					
Lys	Ala	Leu	Gly	Glu	Arg	Ile	Phe	Ala	Leu	Glu	Ala	Thr	Ala	Asp	Gln	
325					330					335					340	
Ser	Ala	Ala	Ser	Phe	Glu	Met	Glu	Met	Ser	Gln	Thr	Gly	Phe	Ser	Ala	
				345					350					355		
His	Tyr	Ser	Gln	Asp	Trp	Val	Met	Leu	Gly	Ala	Val	Gly	Ala	Tyr	Asp	
			360					365					370			
Trp	Asn	Gly	Thr	Val	Val	Met	Gln	Lys	Ala	Asn	Gln	Met	Val	Ile	Pro	
		375					380					385				
His	Asn	Thr	Thr	Phe	Gln	Thr	Glu	Pro	Ala	Lys	Met	Asn	Glu	Pro	Leu	
		390				395					400					
Ala	Ser	Tyr	Leu	Gly	Tyr	Thr	Val	Asn	Ser	Ala	Thr	Ile	Pro	Gly	Asp	
405					410					415					420	
Val	Leu	Tyr	Ile	Ala	Gly	Gln	Pro	Arg	Tyr	Asn	His	Thr	Gly	Gln	Val	
				425					430					435		
Val	Ile	Tyr	Lys	Met	Glu	Asp	Gly	Asn	Ile	Asn	Ile	Leu	Gln	Thr	Leu	
			440					445					450			
Gly	Gly	Glu	Gln	Ile	Gly	Ser	Tyr	Phe	Gly	Ser	Val	Leu	Thr	Thr	Ile	
		455					460					465				
Asp	Ile	Asp	Lys	Asp	Ser	Tyr	Thr	Asp	Leu	Leu	Leu	Val	Gly	Ala	Pro	
		470				475					480					
Met	Tyr	Met	Gly	Thr	Glu	Lys	Glu	Glu	Gln	Gly	Lys	Val	Tyr	Val	Tyr	
485					490					495					500	

Ala Val Asn Gln Thr Arg Phe Glu Tyr Gln Met Ser Leu Glu Pro Ile
505 510 515

Arg Gln Thr Cys Cys Ser Ser Leu Lys Asp Asn Ser Cys Thr Lys Glu
520 525 530

Asn Lys Asn Glu Pro Cys Gly Ala Arg Phe Gly Thr Ala Ile Ala Ala
535 540 545

Val Lys Asp Leu Asn Val Asp Gly Phe Asn Asp Val Val Ile Gly Ala
550 555 560

Pro Leu Glu Asp Asp His Ala Gly Ala Val Tyr Ile Tyr His Gly Ser
565 570 575 580

Gly Lys Thr Ile Arg Glu Ala Tyr Ala Gln Arg Ile Pro Ser Gly Gly
585 590 595

Asp Gly Lys Thr Leu Lys Phe Phe Gly Gln Ser Ile His Gly Glu Met
600 605 610

Asp Leu Asn Gly Asp Gly Leu Thr Asp Val Thr Ile Gly Gly Leu Gly
615 620 625

Gly Ala Ala Leu Phe Trp Ala Arg Asp Val Ala Val Val Lys Val Thr
630 635 640

Met Asn Phe Glu Pro Asn Lys Val Asn Ile Gln Lys Lys Asn Cys Arg
645 650 655 660

Val Glu Gly Lys Glu Thr Val Cys Ile Asn Ala Thr Met Cys Phe His
665 670 675

Val Lys Leu Lys Ser Lys Glu Asp Ser Ile Tyr Glu Ala Asp Leu Gln
680 685 690

Tyr Arg Val Thr Leu Asp Ser Leu Arg Gln Ile Ser Arg Ser Phe Phe
695 700 705

Ser Gly Thr Gln Glu Arg Lys Ile Gln Arg Asn Ile Thr Val Arg Glu
710 715 720

Ser Glu Cys Ile Arg His Ser Phe Tyr Met Leu Asp Lys His Asp Phe
725 730 735 740

Gln Asp Ser Val Arg Val Thr Leu Asp Phe Asn Leu Thr Asp Pro Glu
745 750 755

Asn Gly Pro Val Leu Asp Asp Ala Leu Pro Asn Ser Val His Glu His
760 765 770

Ile Pro Phe Ala Lys Asp Cys Gly Asn Lys Glu Arg Cys Ile Ser Asp
775 780 785

Leu Thr Leu Asn Val Ser Thr Thr Glu Lys Ser Leu Leu Ile Val Lys
790 795 800

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Ser Gln His Asp Lys Phe Asn Val Ser Leu Thr Val Lys Asn Lys Gly
 805 810 815 820
 Asp Ser Ala Tyr Asn Thr Arg Thr Val Val Gln His Ser Pro Asn Leu
 825 830 835
 Ile Phe Ser Gly Ile Glu Glu Ile Gln Lys Asp Ser Cys Glu Ser Asn
 840 845 850
 Gln Asn Ile Thr Cys Arg Val Gly Tyr Pro Phe Leu Arg Ala Gly Glu
 855 860 865
 Thr Val Thr Phe Lys Ile Ile Phe Gln Phe Asn Thr Ser His Leu Ser
 870 875 880
 Glu Asn Ala Ile Ile His Leu Ser Ala Thr Ser Asp Ser Glu Glu Pro
 885 890 895 900
 Leu Glu Ser Leu Asn Asp Asn Glu Val Asn Ile Ser Ile Pro Val Lys
 905 910 915
 Tyr Glu Val Gly Leu Gln Phe Tyr Ser Ser Ala Ser Glu His His Ile
 920 925 930
 Ser Val Ala Ala Asn Glu Thr Ile Pro Glu Phe Ile Asn Ser Thr Glu
 935 940 945
 Asp Ile Gly Asn Glu Ile Asn Val Phe Tyr Thr Ile Arg Lys Arg Gly
 950 955 960
 His Phe Pro Met Pro Glu Leu Gln Leu Ser Ile Ser Phe Pro Asn Leu
 965 970 975 980
 Thr Ala Asp Gly Tyr Pro Val Leu Tyr Pro Ile Gly Trp Ser Ser Ser
 985 990 995
 Asp Asn Val Asn Cys Arg Pro Arg Ser Leu Glu Asp Pro Phe Gly Ile
 1000 1005 1010
 Asn Ser Gly Lys Lys Met Thr Ile Ser Lys Ser Glu Val Leu Lys Arg
 1015 1020 1025
 Gly Thr Ile Gln Asp Cys Ser Ser Thr Cys Gly Val Ala Thr Ile Thr
 1030 1035 1040
 Cys Ser Leu Leu Pro Ser Asp Leu Ser Gln Val Asn Val Ser Leu Leu
 1045 1050 1055 1060
 Leu Trp Lys Pro Thr Phe Ile Arg Ala His Phe Ser Ser Leu Asn Leu
 1065 1070 1075
 Thr Leu Arg Gly Glu Leu Lys Ser Glu Asn Ser Ser Leu Thr Leu Ser
 1080 1085 1090
 Ser Ser Asn Arg Lys Arg Glu Leu Ala Ile Gln Ile Ser Lys Asp Gly
 1095 1100 1105

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 102050-10000000

Leu Pro Gly Arg Val Pro Leu Trp Val Ile Leu Leu Ser Ala Phe Ala
 1110 1115 1120

Gly Leu Leu Leu Leu Met Leu Leu Ile Leu Ala Leu Trp Lys Ile Gly
 1125 1130 1135 1140

Phe Phe Lys Arg Pro Leu Lys Lys Lys Met Glu Lys
 1145 1150

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 49...3591

(D) OTHER INFORMATION:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 136

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCCTGC AAACCCAGCG CAACTACGGT CCCCCGGTCA GACCCAGG ATG GGG CCA	57
Met Gly Pro	
-29	
GAA CGG ACA GGG GCC GCG CCG CTG CCG CTG CTG CTG GTG TTA GCG CTC	105
Glu Arg Thr Gly Ala Ala Pro Leu Pro Leu Leu Leu Val Leu Ala Leu	
-25 -20 -15	
AGT CAA GGC ATT TTA AAT TGT TGT TTG GCC TAC AAT GTT GGT CTC CCA	153
Ser Gln Gly Ile Leu Asn Cys Cys Leu Ala Tyr Asn Val Gly Leu Pro	
-10 -5 1 5	
GAA GCA AAA ATA TTT TCC GGT CCT TCA AGT GAA CAG TTT GGG TAT GCA	201
Glu Ala Lys Ile Phe Ser Gly Pro Ser Ser Glu Gln Phe Gly Tyr Ala	
10 15 20	
GTG CAG CAG TTT ATA AAT CCA AAA GGC AAC TGG TTA CTG GTT GGT TCA	249
Val Gln Gln Phe Ile Asn Pro Lys Gly Asn Trp Leu Leu Val Gly Ser	
25 30 35	

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CCC	TGG	AGT	GGC	TTT	CCT	GAG	AAC	CGA	ATG	GGA	GAT	GTG	TAT	AAA	TGT	297
Pro	Trp	Ser	Gly	Phe	Pro	Glu	Asn	Arg	Met	Gly	Asp	Val	Tyr	Lys	Cys	
40						45				50						
CCT	GTT	GAC	CTA	TCC	ACT	GCC	ACA	TGT	GAA	AAA	CTA	AAT	TTG	CAA	ACT	345
Pro	Val	Asp	Leu	Ser	Thr	Ala	Thr	Cys	Glu	Lys	Leu	Asn	Leu	Gln	Thr	
55					60				65					70		
TCA	ACA	AGC	ATT	CCA	AAT	GTT	ACT	GAG	ATG	AAA	ACC	AAC	ATG	AGC	CTC	393
Ser	Thr	Ser	Ile	Pro	Asn	Val	Thr	Glu	Met	Lys	Thr	Asn	Met	Ser	Leu	
				75				80						85		
GGC	TTG	ATC	CTC	ACC	AGG	AAC	ATG	GGA	ACT	GGA	GGT	TTT	CTC	ACA	TGT	441
Gly	Leu	Ile	Leu	Thr	Arg	Asn	Met	Gly	Thr	Gly	Gly	Phe	Leu	Thr	Cys	
			90					95					100			
GGT	CCT	CTG	TGG	GCA	CAG	CAA	TGT	GGG	AAT	CAG	TAT	TAC	ACA	ACG	GGT	489
Gly	Pro	Leu	Trp	Ala	Gln	Gln	Cys	Gly	Asn	Gln	Tyr	Tyr	Thr	Thr	Gly	
	105						110					115				
GTG	TGT	TCT	GAC	ATC	AGT	CCT	GAT	TTT	CAG	CTC	TCA	GCC	AGC	TTC	TCA	537
Val	Cys	Ser	Asp	Ile	Ser	Pro	Asp	Phe	Gln	Leu	Ser	Ala	Ser	Phe	Ser	
	120					125					130					
CCT	GCA	ACT	CAG	CCC	TGC	CCT	TCC	CTC	ATA	GAT	GTT	GTG	GTT	GTG	TGT	585
Pro	Ala	Thr	Gln	Pro	Cys	Pro	Ser	Leu	Ile	Asp	Val	Val	Val	Val	Cys	
135					140					145					150	
GAT	GAA	TCA	AAT	AGT	ATT	TAT	CCT	TGG	GAT	GCA	GTA	AAG	AAT	TTT	TTG	633
Asp	Glu	Ser	Asn	Ser	Ile	Tyr	Pro	Trp	Asp	Ala	Val	Lys	Asn	Phe	Leu	
				155				160						165		
GAA	AAA	TTT	GTA	CAA	GGC	CTT	GAT	ATA	GGC	CCC	ACA	AAG	ACA	CAG	GTG	681
Glu	Lys	Phe	Val	Gln	Gly	Leu	Asp	Ile	Gly	Pro	Thr	Lys	Thr	Gln	Val	
			170					175					180			
GGG	TTA	ATT	CAG	TAT	GCC	AAT	AAT	CCA	AGA	GTT	GTG	TTT	AAC	TTG	AAC	729
Gly	Leu	Ile	Gln	Tyr	Ala	Asn	Asn	Pro	Arg	Val	Val	Phe	Asn	Leu	Asn	
		185					190					195				
ACA	TAT	AAA	ACC	AAA	GAA	GAA	ATG	ATT	GTA	GCA	ACA	TCC	CAG	ACA	TCC	777
Thr	Tyr	Lys	Thr	Lys	Glu	Glu	Met	Ile	Val	Ala	Thr	Ser	Gln	Thr	Ser	
	200					205					210					
CAA	TAT	GGT	GGG	GAC	CTC	ACA	AAC	ACA	TTC	GGA	GCA	ATT	CAA	TAT	GCA	825
Gln	Tyr	Gly	Gly	Asp	Leu	Thr	Asn	Thr	Phe	Gly	Ala	Ile	Gln	Tyr	Ala	
215					220					225				230		
AGA	AAA	TAT	GCC	TAT	TCA	GCA	GCT	TCT	GGT	GGG	CGA	CGA	AGT	GCT	ACG	873
Arg	Lys	Tyr	Ala	Tyr	Ser	Ala	Ala	Ser	Gly	Gly	Arg	Arg	Ser	Ala	Thr	
			235					240						245		
AAA	GTA	ATG	GTA	GTT	GTA	ACT	GAC	GGT	GAA	TCA	CAT	GAT	GGT	TCA	ATG	921
Lys	Val	Met	Val	Val	Val	Thr	Asp	Gly	Glu	Ser	His	Asp	Gly	Ser	Met	
			250					255					260			

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TTG AAA GCT GTG ATT GAT CAA TGC AAC CAT GAC AAT ATA CTG AGG TTT	969
Leu Lys Ala Val Ile Asp Gln Cys Asn His Asp Asn Ile Leu Arg Phe	
265 270 275	
GGC ATA GCA GTT CTT GGG TAC TTA AAC AGA AAC GCC CTT GAT ACT AAA	1017
Gly Ile Ala Val Leu Gly Tyr Leu Asn Arg Asn Ala Leu Asp Thr Lys	
280 285 290	
AAT TTA ATA AAA GAA ATA AAA GCG ATC GCT AGT ATT CCA ACA GAA AGA	1065
Asn Leu Ile Lys Glu Ile Lys Ala Ile Ala Ser Ile Pro Thr Glu Arg	
295 300 305 310	
TAC TTT TTC AAT GTG TCT GAT GAA GCA GCT CTA CTA GAA AAG GCT GGG	1113
Tyr Phe Phe Asn Val Ser Asp Glu Ala Ala Leu Leu Glu Lys Ala Gly	
315 320 325	
ACA TTA GGA GAA CAA ATT TTC AGC ATT GAA GGT ACT GTT CAA GGA GGA	1161
Thr Leu Gly Glu Gln Ile Phe Ser Ile Glu Gly Thr Val Gln Gly Gly	
330 335 340	
GAC AAC TTT CAG ATG GAA ATG TCA CAA GTG GGA TTC AGT GCA GAT TAC	1209
Asp Asn Phe Gln Met Glu Met Ser Gln Val Gly Phe Ser Ala Asp Tyr	
345 350 355	
TCT TCT CAA AAT GAT ATT CTG ATG CTG GGT GCA GTG GGA GCT TTT GGC	1257
Ser Ser Gln Asn Asp Ile Leu Met Leu Gly Ala Val Gly Ala Phe Gly	
360 365 370	
TGG AGT GGG ACC ATT GTC CAG AAG ACA TCT CAT GGC CAT TTG ATC TTT	1305
Trp Ser Gly Thr Ile Val Gln Lys Thr Ser His Gly His Leu Ile Phe	
375 380 385 390	
CCT AAA CAA GCC TTT GAC CAA ATT CTG CAG GAC AGA AAT CAC AGT TCA	1353
Pro Lys Gln Ala Phe Asp Gln Ile Leu Gln Asp Arg Asn His Ser Ser	
395 400 405	
TAT TTA GGT TAC TCT GTG GCT GCA ATT TCT ACT GGA GAA AGC ACT CAC	1401
Tyr Leu Gly Tyr Ser Val Ala Ala Ile Ser Thr Gly Glu Ser Thr His	
410 415 420	
TTT GTT GCT GGT GCT CCT CGG GCA AAT TAT ACC GGC CAG ATA GTG CTA	1449
Phe Val Ala Gly Ala Pro Arg Ala Asn Tyr Thr Gly Gln Ile Val Leu	
425 430 435	
TAT AGT GTG AAT GAG AAT GGC AAT ATC ACG GTT ATT CAG GCT CAC CGA	1497
Tyr Ser Val Asn Glu Asn Gly Asn Ile Thr Val Ile Gln Ala His Arg	
440 445 450	
GGT GAC CAG ATT GGC TCC TAT TTT GGT AGT GTG CTG TGT TCA GTT GAT	1545
Gly Asp Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Cys Ser Val Asp	
455 460 465 470	
GTG GAT AAA GAC ACC ATT ACA GAC GTG CTC TTG GTA GGT GCA CCA ATG	1593
Val Asp Lys Asp Thr Ile Thr Asp Val Leu Leu Val Gly Ala Pro Met	
475 480 485	

TAC	ATG	AGT	GAC	CTA	AAG	AAA	GAG	GAA	GGA	AGA	GTC	TAC	CTG	TTT	ACT	1641
Tyr	Met	Ser	Asp	Leu	Lys	Lys	Glu	Glu	Gly	Arg	Val	Tyr	Leu	Phe	Thr	
			490					495					500			
ATC	AAA	AAG	GGC	ATT	TTG	GGT	CAG	CAC	CAA	TTT	CTT	GAA	GGC	CCC	GAG	1689
Ile	Lys	Lys	Gly	Ile	Leu	Gly	Gln	His	Gln	Phe	Leu	Glu	Gly	Pro	Glu	
		505					510					515				
GGC	ATT	GAA	AAC	ACT	CGA	TTT	GGT	TCA	GCA	ATT	GCA	GCT	CTT	TCA	GAC	1737
Gly	Ile	Glu	Asn	Thr	Arg	Phe	Gly	Ser	Ala	Ile	Ala	Ala	Leu	Ser	Asp	
	520					525					530					
ATC	AAC	ATG	GAT	GGC	TTT	AAT	GAT	GTG	ATT	GTT	GGT	TCA	CCA	CTA	GAA	1785
Ile	Asn	Met	Asp	Gly	Phe	Asn	Asp	Val	Ile	Val	Gly	Ser	Pro	Leu	Glu	
535					540					545					550	
AAT	CAG	AAT	TCT	GGA	GCT	GTA	TAC	ATT	TAC	AAT	GGT	CAT	CAG	GGC	ACT	1833
Asn	Gln	Asn	Ser	Gly	Ala	Val	Tyr	Ile	Tyr	Asn	Gly	His	Gln	Gly	Thr	
			555						560					565		
ATC	CGC	ACA	AAG	TAT	TCC	CAG	AAA	ATC	TTG	GGA	TCC	GAT	GGA	GCC	TTT	1881
Ile	Arg	Thr	Lys	Tyr	Ser	Gln	Lys	Ile	Leu	Gly	Ser	Asp	Gly	Ala	Phe	
			570					576					580			
AGG	AGC	CAT	CTC	CAG	TAC	TTT	GGG	AGG	TCC	TTG	GAT	GGC	TAT	GGA	GAT	1929
Arg	Ser	His	Leu	Gln	Tyr	Phe	Gly	Arg	Ser	Leu	Asp	Gly	Tyr	Gly	Asp	
		585					590					595				
TTA	AAT	GGG	GAT	TCC	ATC	ACC	GAT	GTG	TCT	ATT	GGT	GCC	TTT	GGA	CAA	1977
Leu	Asn	Gly	Asp	Ser	Ile	Thr	Asp	Val	Ser	Ile	Gly	Ala	Phe	Gly	Gln	
	600					605					610					
GTG	GTT	CAA	CTC	TGG	TCA	CAA	AGT	ATT	GCT	GAT	GTA	GCT	ATA	GAA	GCT	2025
Val	Val	Gln	Leu	Trp	Ser	Gln	Ser	Ile	Ala	Asp	Val	Ala	Ile	Glu	Ala	
615					620					625					630	
TCA	TTC	ACA	CCA	GAA	AAA	ATC	ACT	TTG	GTC	AAC	AAG	AAT	GCT	CAG	ATA	2073
Ser	Phe	Thr	Pro	Glu	Lys	Ile	Thr	Leu	Val	Asn	Lys	Asn	Ala	Gln	Ile	
			635						640					645		
ATT	CTC	AAA	CTC	TGC	TTC	AGT	GCA	AAG	TTC	AGA	CCT	ACT	AAG	CAA	AAC	2121
Ile	Leu	Lys	Leu	Cys	Phe	Ser	Ala	Lys	Phe	Arg	Pro	Thr	Lys	Gln	Asn	
		650						655					660			
AAT	CAA	GTG	GCC	ATT	GTA	TAT	AAC	ATC	ACA	CTT	GAT	GCA	GAT	GGA	TTT	2169
Asn	Gln	Val	Ala	Ile	Val	Tyr	Asn	Ile	Thr	Leu	Asp	Ala	Asp	Gly	Phe	
		665					670					675				
TCA	TCC	AGA	GTA	ACC	TCC	AGG	GGG	TTA	TTT	AAA	GAA	AAC	AAT	GAA	AGG	2217
Ser	Ser	Arg	Val	Thr	Ser	Arg	Gly	Leu	Phe	Lys	Glu	Asn	Asn	Glu	Arg	
		680				685					690					
TGC	CTG	CAG	AAG	AAT	ATG	GTA	GTA	AAT	CAA	GCA	CAG	AGT	TGC	CCC	GAG	2265

CAC His	ATC Ile	ATT Ile	TAT Tyr	ATA Ile 725	CAG Gln	GAG Glu	CCC Pro	TCT Ser	GAT Asp 730	GTT Val	GTC Val	AAC Asn	TCT Ser	TTG Leu 735	GAT Asp	2313
TTG Leu	CGT Arg	GTG Val	GAC Asp 740	ATC Ile	AGT Ser	CTG Leu	GAA Glu 745	AAC Asn	CCT Pro	GGC Gly	ACT Thr	AGC Ser	CCT Pro 750	GCC Ala	CTT Leu	2361
GAA Glu	GCC Ala	TAT Tyr 755	TCT Ser	GAG Glu	ACT Thr	GCC Ala	AAG Lys 760	GTC Val	TTC Phe	AGT Ser	ATT Ile	CCT Pro 765	TTC Phe	CAC His	AAA Lys	2409
GAC Asp	TGT Cys 760	GGT Gly	GAG Glu	GAT Asp	GGA Gly	CTT Leu 765	TGC Cys	ATT Ile	TCT Ser	GAT Asp	CTA Leu 770	GTC Val	CTA Leu	GAT Asp	GTC Val	2457
CGA Arg 775	CAA Gln	ATA Ile	CCA Pro	GCT Ala	GCT Ala 780	CAA Gln	GAA Glu	CAA Gln	CCC Pro	TTT Phe 785	ATT Ile	GTC Val	AGC Ser	AAC Asn	CAA Gln 790	2505
AAC Asn	AAA Lys	AGG Arg	TTA Leu	ACA Thr 795	TTT Phe	TCA Ser	GTA Val	ACA Thr	CTG Leu 800	AAA Lys	AAT Asn	AAA Lys	AGG Arg	GAA Glu 805	AGT Ser	2553
GCA Ala	TAC Tyr	AAC Asn 810	ACT Thr	GGA Gly	ATT Ile	GTT Val	GTT Val	GAT Asp 815	TTT Phe	TCA Ser	GAA Glu	AAC Asn	TTG Leu 820	TTT Phe	TTT Phe	2601
GCA Ala	TCA Ser	TTC Phe 825	TCC Ser	CTA Leu	CCG Pro	GTT Val	GAT Asp 830	GGG Gly	ACA Thr	GAA Glu	GTA Val	ACA Thr 835	TGC Cys	CAG Gln	GTG Val	2649
GCT Ala	GCA Ala 840	TCT Ser	CAG Gln	AAG Lys	TCT Ser	GTT Val 845	GCC Ala	TGC Cys	GAT Asp	GTA Val	GGC Gly 850	TAC Tyr	CCT Pro	GCT Ala	TTA Leu	2697
AAG Lys 855	AGA Arg	GAA Glu	CAA Gln	CAG Gln 860	GTG Val	ACT Thr	TTT Phe	ACT Thr	ATT Ile	AAC Asn 865	TTT Phe	GAC Asp	TTC Phe	AAT Asn	CTT Leu 870	2745
CAA Gln	AAC Asn	CTT Leu	CAG Gln 875	AAT Asn	CAG Gln	GCG Ala	TCT Ser	CTC Leu	AGT Ser 880	TTC Phe	CAA Gln	GCC Ala	TTA Leu	AGT Ser 885	GAA Glu	2793
AGC Ser	CAA Gln	GAA Glu	GAA Glu 890	AAC Asn	AAG Lys	GCT Ala	GAT Asp 895	AAT Asn	TTG Leu	GTC Val	AAC Asn	CTC Leu	AAA Lys 900	ATT Ile	CCT Pro	2841
CTC Leu	CTG Leu	TAT Tyr 905	GAT Asp	GCT Ala	GAA Glu	ATT Ile	CAC His 910	TTA Leu	ACA Thr	AGA Arg	TCT Ser	ACC Thr 915	AAC Asn	ATA Ile	AAT Asn	2889
TTT Phe	TAT Tyr 920	GAA Glu	ATC Ile	TCT Ser	TCG Ser	GAT Asp 925	GGG Gly	AAT Asn	GTT Val	CCT Pro	TCA Ser 930	ATC Ile	GTG Val	CAC His	AGT Ser	2937

[illegible]

TTT	GAA	GAT	GTT	GGT	CCA	AAA	TTC	ATC	TTC	TCC	CTG	AAG	GTA	ACA	ACA	2985
Phe	Glu	Asp	Val	Gly	Pro	Lys	Phe	Ile	Phe	Ser	Leu	Lys	Val	Thr	Thr	
935					940					945					950	
GGA	AGT	GTT	CCA	GTA	AGC	ATG	GCA	ACT	GTA	ATC	ATC	CAC	ATC	CCT	CAG	3033
Gly	Ser	Val	Pro	Val	Ser	Met	Ala	Thr	Val	Ile	Ile	His	Ile	Pro	Gln	
				955					960					965		
TAT	ACC	AAA	GAA	AAG	AAC	CCA	CTG	ATG	TAC	CTA	ACT	GGG	GTG	CAA	ACA	3081
Tyr	Thr	Lys	Glu	Lys	Asn	Pro	Leu	Met	Tyr	Leu	Thr	Gly	Val	Gln	Thr	
			970					975					980			
GAC	AAG	GCT	GGT	GAC	ATC	AGT	TGT	AAT	GCA	GAT	ATC	AAT	CCA	CTG	AAA	3129
Asp	Lys	Ala	Gly	Asp	Ile	Ser	Cys	Asn	Ala	Asp	Ile	Asn	Pro	Leu	Lys	
		985					990					995				
ATA	GGA	CAA	ACA	TCT	TCT	TCT	GTA	TCT	TTC	AAA	AGT	GAA	AAT	TTC	AGG	3177
Ile	Gly	Gln	Thr	Ser	Ser	Ser	Val	Ser	Phe	Lys	Ser	Glu	Asn	Phe	Arg	
	1000					1005					1010					
CAC	ACC	AAA	GAA	TTG	AAC	TGC	AGA	ACT	GCT	TCC	TGT	AGT	AAT	GTT	ACC	3225
His	Thr	Lys	Glu	Leu	Asn	Cys	Arg	Thr	Ala	Ser	Cys	Ser	Asn	Val	Thr	
1015					1020					1025					1030	
TGC	TGG	TTG	AAA	GAC	GTT	CAC	ATG	AAA	GGA	GAA	TAC	TTT	GTT	AAT	GTG	3273
Cys	Trp	Leu	Lys	Asp	Val	His	Met	Lys	Gly	Glu	Tyr	Phe	Val	Asn	Val	
				1035					1040					1045		
ACT	ACC	AGA	ATT	TGG	AAC	GGG	ACT	TTC	GCA	TCA	TCA	ACG	TTC	CAG	ACA	3321
Thr	Thr	Arg	Ile	Trp	Asn	Gly	Thr	Phe	Ala	Ser	Ser	Thr	Phe	Gln	Thr	
			1050					1055					1060			
GTA	CAG	CTA	ACG	GCA	GCT	GCA	GAA	ATC	AAC	ACC	TAT	AAC	CCT	GAG	ATA	3369
Val	Gln	Leu	Thr	Ala	Ala	Ala	Glu	Ile	Asn	Thr	Tyr	Asn	Pro	Glu	Ile	
			1065				1070					1075				
TAT	GTG	ATT	GAA	GAT	AAC	ACT	GTT	ACG	ATT	CCC	CTG	ATG	ATA	ATG	AAA	3417
Tyr	Val	Ile	Glu	Asp	Asn	Thr	Val	Thr	Ile	Pro	Leu	Met	Ile	Met	Lys	
	1080					1085					1090					
CCT	GAT	GAG	AAA	GCC	GAA	GTA	CCA	ACA	GGA	GTT	ATA	ATA	GGA	AGT	ATA	3465
Pro	Asp	Glu	Lys	Ala	Glu	Val	Pro	Thr	Gly	Val	Ile	Ile	Gly	Ser	Ile	
1095					1100					1105					1110	
ATT	GCT	GGA	ATC	CTT	TTG	CTG	TTA	GCT	CTG	GTT	GCA	ATT	TTA	TGG	AAG	3513
Ile	Ala	Gly	Ile	Leu	Leu	Leu	Leu	Ala	Leu	Val	Ala	Ile	Leu	Trp	Lys	
				1115					1120					1125		
CTC	GGC	TTC	TTC	AAA	AGA	AAA	TAT	GAA	AAG	ATG	ACC	AAA	AAT	CCA	GAT	3561
Leu	Gly	Phe	Phe	Lys	Arg	Lys	Tyr	Glu	Lys	Met	Thr	Lys	Asn	Pro	Asp	
			1130					1135					1140			
GAG																

GGGAACCGGC AGCATCCCAG CCAGGGTTTG CTGTTTGCCT GCATGGATTT CTTTTTAAAT 3675
 CCCATATTTT TTTTATCATG TCGTAGGTAA ACTAACCTGG TATTTTAAGA GAAAACTGCA 3735
 GGTCAAGTTT GATGAAGAAA TTGTGGGGGG TGGGGGAGGT GCGGGGGGCA GGTAGGGAAA 3795
 TAATAGGGAA AATACCTATT TTATATGATG GGGGAAAAAA AGTAATCTTT AAACCTGGCTG 3855
 GCCCAGAGTT TACATTCTAA TTTGCATTGT GTCAGAAACA TGAAATGCTT CCAAGCATGA 3915
 CAACTTTTAA AGAAAAATAT GATACTCTCA GATTTTAAAG GGGAAAACTG TTCTCTTTAA 3975
 AATATTTGTC TTTAAACAGC AACTACAGAA GTGGAAGTGC TTGATATGTA AGTACTTCCA 4035
 CTTGTGTATA TTTTAAATGAA TATTGATGTT AACAAGAGGG GAAAACAAAA CACAGGTTTT 4095
 TTCAATTTAT GCTGCTCATC CAAAGTTGCC ACAGATGATA CTTCCAAGTG ATAATTTTAT 4155
 TTATAAACTA GGTAAAATTT GTTGTGTTGTT CCTTTTATAC CACGGCTGCC CCTTCCACAC 4215
 CCCATCTTGC TCTAATGATC AAAACATGCT TGAATAACTG AGCTTAGAGT ATACCTCCTA 4275
 TATGTCCATT TAAGTTAGGA GAGGGGGCGA TATAGAGACT AAGGCACAAA ATTTTGTTTA 4335
 AAACCTCAGAA TATAACATTT ATGTAAAATC CCATCTGCTA GAAGCCCATC CTGTGCCAGA 4395
 GGAAGGAAAA GGAGGAAATT TCCTTTCTCT TTTAGGAGGC ACAACAGTTC TCTTCTAGGA 4455
 TTTGTTTGGC TGACTGGCAG TAACCTAGTG AATTTTGTAA AGATGAGTAA TTTCTTTGGC 4515
 AACCTTCCTC CTCCCTTACT GAACCACTCT CCCACCTCCT GGTGGTACCA TTATTATAGA 4575
 AGCCCTCTAC AGCCTGACTT TCTCTCCAGC GGTCCAAAGT TATCCCCTCC TTTACCCCTC 4635
 ATCCAAAGTT CCCACTCCTT CAGGACAGCT GCTGTGCATT AGATATTAGG GGGGAAAGTC 4695
 ATCTGTTTAA TTTACACACT TGCATGAATT ACTGTATATA AACTCCTTAA CTTCAAGGAG 4755
 CTATTTTTCAT TTAGTGCTAA ACAAGTAAGA AAAATAAGCT AGAGTGAATT TCTAAATGTT 4815
 GGAATGTTAT GGGATGTAAA CAATGTAAAG TAAAACACTC TCAGGATTTC ACCAGAAGTT 4875
 ACAGATGAGG CACTGGAAAC CACCACCAAA TTAGCAGGTG CACCTTCTGT GGCTGTCTTG 4935
 TTTCTGAAGT ACTTTTTCTT CCACAAGAGT GAATTTGACC TAGGCAAGTT TGTTCAAAAG 4995
 GTAGATCCTG AGATGATTTG GTCAGATTGG GATAAGGCC AGCAATCTGC ATTTTAAACAA 5055
 GCACCCAGT CACTAGGATG CAGATGGACC ACACTTTGAG AAACACCACC CATTTCTACT 5115
 TTTTGCACCT TATTTTCTCT GTTCCTGAGC CCCCACATTC TCTAGGAGAA ACTTAGATTA 5175
 AAATTCACAG AACTACATA TCTAAAGCTT TGACAAGTCC TTGACCTCTA TAAACTTCAG 5235
 AGTCCTCATT ATAAAATGGG AAGACTGAGC TGGAGTTCAG CAGTGATGCT TTTTAGTTTT 5295
 AAAAGTCTAT GATCTGATCT GGACTTCCTA TAATACAAAT ACACAATCCT CCAAGAATTT 5355
 GACTTGGAAG AGGAATTC 5373

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Pro Glu Arg Thr Gly Ala Ala Pro Leu Pro Leu Leu Val
 -29 -25 -20 -15

Leu Ala Leu Ser Gln Gly Ile Leu Asn Cys Cys Leu Ala Tyr Asn Val
 -10 -5 1

Gly Leu Pro Glu Ala Lys Ile Phe Ser Gly Pro Ser Ser Glu Gln Phe
 5 10 15

Gly 20	Tyr	Ala	Val	Gln	Gln	Phe	Ile	Asn	Pro	Lys	Gly	Asn	Trp	Leu	Leu
				25				30				35			
Val	Gly	Ser	Pro	Trp	Ser	Gly	Phe	Pro	Glu	Asn	Arg	Met	Gly	Asp	Val
				40				45				50			
Tyr	Lys	Cys	Pro	Val	Asp	Leu	Ser	Thr	Ala	Thr	Cys	Glu	Lys	Leu	Asn
				55				60				65			
Leu	Gln	Thr	Ser	Thr	Ser	Ile	Pro	Asn	Val	Thr	Glu	Met	Lys	Thr	Asn
				70				75				80			
Met	Ser	Leu	Gly	Leu	Ile	Leu	Thr	Arg	Asn	Met	Gly	Thr	Gly	Gly	Phe
				85				90				95			
Leu	Thr	Cys	Gly	Pro	Leu	Trp	Ala	Gln	Gln	Cys	Gly	Asn	Gln	Tyr	Tyr
100				105				110				115			
Thr	Thr	Gly	Val	Cys	Ser	Asp	Ile	Ser	Pro	Asp	Phe	Gln	Leu	Ser	Ala
				120				125				130			
Ser	Phe	Ser	Pro	Ala	Thr	Gln	Pro	Cys	Pro	Ser	Leu	Ile	Asp	Val	Val
				135				140				145			
Val	Val	Cys	Asp	Glu	Ser	Asn	Ser	Ile	Tyr	Pro	Trp	Asp	Ala	Val	Lys
				150				155				160			
Asn	Phe	Leu	Glu	Lys	Phe	Val	Gln	Gly	Leu	Asp	Ile	Gly	Pro	Thr	Lys
				165				170				175			
Thr	Gln	Val	Gly	Leu	Ile	Gln	Tyr	Ala	Asn	Asn	Pro	Arg	Val	Val	Phe
180				185				190				195			
Asn	Leu	Asn	Thr	Tyr	Lys	Thr	Lys	Glu	Glu	Met	Ile	Val	Ala	Thr	Ser
				200				205				210			
Gln	Thr	Ser	Gln	Tyr	Gly	Gly	Asp	Leu	Thr	Asn	Thr	Phe	Gly	Ala	Ile
				215				220				225			
Gln	Tyr	Ala	Arg	Lys	Tyr	Ala	Tyr	Ser	Ala	Ala	Ser	Gly	Gly	Arg	Arg
				230				235				240			
Ser	Ala	Thr	Lys	Val	Met	Val	Val	Val	Thr	Asp	Gly	Glu	Ser	His	Asp
				245				250				255			
Gly	Ser	Met	Leu	Lys	Ala	Val	Ile	Asp	Gln	Cys	Asn	His	Asp	Asn	Ile
260				265				270				275			
Leu	Arg	Phe	Gly	Ile	Ala	Val	Leu	Gly	Tyr	Leu	Asn	Arg	Asn	Ala	Leu
				280				285				290			
Asp	Thr	Lys	Asn	Leu	Ile	Lys	Glu	Ile	Lys	Ala	Ile	Ala	Ser	Ile	Pro
				295				300				305			
Thr	Glu	Arg	Tyr	Phe	Phe	Asn	Val	Ser	Asp	Glu	Ala	Ala	Leu	Leu	Glu
				310				315				320			

Lys Ala Gly Thr Leu Gly Glu Gln Ile Phe Ser Ile Glu Gly Thr Val
 325 330 335
 Gln Gly Gly Asp Asn Phe Gln Met Glu Met Ser Gln Val Gly Phe Ser
 340 345 350 355
 Ala Asp Tyr Ser Ser Gln Asn Asp Ile Leu Met Leu Gly Ala Val Gly
 360 365 370
 Ala Phe Gly Trp Ser Gly Thr Ile Val Gln Lys Thr Ser His Gly His
 375 380 385
 Leu Ile Phe Pro Lys Gln Ala Phe Asp Gln Ile Leu Gln Asp Arg Asn
 390 395 400
 His Ser Ser Tyr Leu Gly Tyr Ser Val Ala Ala Ile Ser Thr Gly Glu
 405 410 415
 Ser Thr His Phe Val Ala Gly Ala Pro Arg Ala Asn Tyr Thr Gly Gln
 420 425 430 435
 Ile Val Leu Tyr Ser Val Asn Glu Asn Gly Asn Ile Thr Val Ile Gln
 440 445 450
 Ala His Arg Gly Asp Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Cys
 455 460 465
 Ser Val Asp Val Asp Lys Asp Thr Ile Thr Asp Val Leu Leu Val Gly
 470 475 480
 Ala Pro Met Tyr Met Ser Asp Leu Lys Lys Glu Glu Gly Arg Val Tyr
 485 490 495
 Leu Phe Thr Ile Lys Lys Gly Ile Leu Gly Gln His Gln Phe Leu Glu
 500 505 510 515
 Gly Pro Glu Gly Ile Glu Asn Thr Arg Phe Gly Ser Ala Ile Ala Ala
 520 525 530
 Leu Ser Asp Ile Asn Met Asp Gly Phe Asn Asp Val Ile Val Gly Ser
 535 540 545
 Pro Leu Glu Asn Gln Asn Ser Gly Ala Val Tyr Ile Tyr Asn Gly His
 550 555 560
 Gln Gly Thr Ile Arg Thr Lys Tyr Ser Gln Lys Ile Leu Gly Ser Asp
 565 570 575
 Gly Ala Phe Arg Ser His Leu Gln Tyr Phe Gly Arg Ser Leu Asp Gly
 580 585 590 595
 Tyr Gly Asp Leu Asn Gly Asp Ser Ile Thr Asp Val Ser Ile Gly Ala
 600 605 610
 Phe Gly Gln Val Val Gln Leu Trp Ser Gln Ser Ile Ala Asp Val Ala
 615 620 625

102050-40000000

Figure 1. The 12-lead ECG of the patient. The ECG shows a sinus rhythm with a heart rate of 75 beats per minute. The P waves are upright and of normal amplitude in leads I, II, III, aVR, aVL, and aVF. The QRS complex is narrow and of normal amplitude. The T waves are upright and of normal amplitude in leads I, II, III, aVR, aVL, and aVF. The ST segments are isoelectric in all leads.

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) **FRAGMENT TYPE:**

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCAGAGTCAC TCTCACAGAG

20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) **FRAGMENT TYPE:**

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CACAGCGTAC ACGTACACC

19

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CACTTATAGA CATCTCCAG

19

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATCCATGTT GATGTCTG

18

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CATGTGATTC ACCGTCAG

18

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCATATTGAA TTGCTCCGAA TGTG

24

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCGTATGCA CAACGCA

17

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCGACAGCTG ACCAGTCAGC A

21

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CACTCCTCCA CAGCTCCT

18

T020501-40000000

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- ```
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACATGTACTC ACTGG

15

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- ```
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTCACATGTG GTCCTCTG

18

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- ```
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTCCTGTTGA CCTATCCACT GC

22